

BLAST Basic Local Alignment Search Tool

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Nucleotide Sequence (20 letters)

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|6069

Description

None

Molecule type

nucleic acid

Query Length

20

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTX 2.2.21+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastx
Query range	0-56
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	12
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40

Database

Posted date	Aug 30, 2009 5:41 PM
Number of letters	3,288,814,006
Number of sequences	9,617,243
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.277865	0.267
K	0.0810434	0.041
H	0.188476	0.14

Results Statistics

Length adjustment	0
Effective length of query	20
Effective length of database	3288814006
Effective search space	19732884036
Effective search space used	19732884036

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Descriptions

Alignments